RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/559,431 _____

Source: _____ TFWO _____

Date Processed by STIC: _____ 12/20/2005 _____

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: _10/559, 431_

CRF Edit Date: _12/20/2005_
Edited by: _DA_

____ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

____ Corrected the SEQ ID NO. Sequence numbers edited were:

_____

____ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

__✓__ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

____ Inserted mandatory headings/numeric identifiers, specifically:

_____

____ Moved responses to same line as heading/numeric identifier, specifically:

_____

____ Other:

_____
_____
_____

Revised 09/09/2003

IFWP

```
RAW SEQUENCE LISTING                      DATE: 12/20/2005
PATENT APPLICATION:  US/10/559,431        TIME: 13:16:57

Input Set : A:\pto.da.txt
Output Set: N:\CRF4\12202005\J559431.raw
```

```
     4 <110> APPLICANT: BIOMERIEUX
     5       INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
     7 <120> TITLE OF INVENTION: Composition comprising the polyprotein NS3/NS4 and the
polypeptide NS5b
     8       of HCV, expression vectors including the corresponding nucleic sequences and
     9       their therapeutic use
    11 <130> FILE REFERENCE: ADENOVIR
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/559,431
C--> 13 <141> CURRENT FILING DATE: 2005-12-05
    13 <160> NUMBER OF SEQ ID NOS: 27
    15 <170> SOFTWARE: PatentIn version 3.1
    17 <210> SEQ ID NO: 1
    18 <211> LENGTH: 2844
    19 <212> TYPE: DNA
    20 <213> ORGANISM: Artificial sequence
    22 <220> FEATURE:
    23 <223> OTHER INFORMATION: sequence coding for NS3NS4
    25 <220> FEATURE:
    26 <221> NAME/KEY: CDS
    27 <222> LOCATION: (1)..(2844)
    28 <223> OTHER INFORMATION:
W--> 30 <400> 1
    31 atg gcg cct atc acg gcc tat tcc caa caa acg cgg ggc ctg ctt ggc      48
    32 Met Ala Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly
    33 1               5                   10                  15
    35 tgt atc atc act agc ctc aca ggt cgg gac aag aac cag gtc gat ggg      96
    36 Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Asp Gly
    37             20                  25                  30
    39 gag gtt cag gtg ctc tcc acc gca acg caa tct ttc ctg gcg acc tgc     144
    40 Glu Val Gln Val Leu Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys
    41             35                  40                  45
    43 gtc aat ggc gtg tgt tgg acc gtc tac cat ggt gcc ggc tcg aag acc     192
    44 Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr
    45         50                  55                  60
    47 ctg gcc ggc ccg aag ggt cca atc acc caa atg tac acc aat gta gac     240
    48 Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp
    49 65                  70                  75                  80
    51 cag gac ctc gtc ggc tgg ccg gcg ccc ccc ggg gcg cgc tcc atg aca     288
    52 Gln Asp Leu Val Gly Trp Pro Ala Pro Pro Gly Ala Arg Ser Met Thr
    53                 85                  90                  95
    55 ccg tgc acc tgc ggc agc tcg gac ctt tac ttg gtc acg agg cat gcc     336
    56 Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala
    57             100                 105                 110
    59 gat gtc att ccg gtg cgc cgg cga ggc gac agc agg ggg agt cta ctc     384
```

```
60 Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu
61         115                 120                 125
63 tcc cct agg ccc gtc tcc tac ctg aag ggc tcc tcg ggt gga cca ctg       432
64 Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu
65         130                 135                 140
67 ctt tgc cct tcg ggg cac gtt gta ggc atc ttc cgg gct gct gtg tgc       480
68 Leu Cys Pro Ser Gly His Val Val Gly Ile Phe Arg Ala Ala Val Cys
69 145                 150                 155                 160
71 acc cgg ggg gtt gcg aag gcg gtg gac ttc ata ccc gtt gag tct atg       528
72 Thr Arg Gly Val Ala Lys Ala Val Asp Phe Ile Pro Val Glu Ser Met
73                 165                 170                 175
75 gaa act acc atg cgg tct ccg gtc ttc aca gac aac tca tcc cct ccg       576
76 Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro
77                 180                 185                 190
79 gcc gta ccg caa aca ttc caa gtg gca cat tta cac gct ccc act ggc       624
80 Ala Val Pro Gln Thr Phe Gln Val Ala His Leu His Ala Pro Thr Gly
81         195                 200                 205
83 agc ggc aag agc acc aaa gtg ccg gct gca tat gca gcc caa ggg tac       672
84 Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr
85         210                 215                 220
87 aag gtg ctc gtc cta aac ccg tcc gtt gct gcc aca ttg ggc ttt gga       720
88 Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly
89 225                 230                 235                 240
91 gcg tat atg tcc aag gca cat ggc atc gag cct aac atc aga act ggg       768
92 Ala Tyr Met Ser Lys Ala His Gly Ile Glu Pro Asn Ile Arg Thr Gly
93                 245                 250                 255
95 gta agg acc atc acc acg ggc ggc ccc atc acg tac tcc acc tat ggc       816
96 Val Arg Thr Ile Thr Thr Gly Gly Pro Ile Thr Tyr Ser Thr Tyr Gly
97                 260                 265                 270
99 aag ttc ctt gcc gac ggt gga tgc tcc ggg ggc gcc tat gac atc ata       864
100 Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile
101         275                 280                 285
103 ata tgt gac gaa tgc cac tca act gac tgg aca acc atc ttg ggc atc       912
104 Ile Cys Asp Glu Cys His Ser Thr Asp Trp Thr Thr Ile Leu Gly Ile
105         290                 295                 300
107 ggc aca gtc ctg gat cag gca gag acg gct gga gcg cgg ctc gtc gtg       960
108 Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val
109 305                 310                 315                 320
111 ctc gcc acc gcc acg cct ccg gga tcg atc acc gtg cca cac ccc aac      1008
112 Leu Ala Thr Ala Thr Pro Pro Gly Ser Ile Thr Val Pro His Pro Asn
113                 325                 330                 335
115 atc gag gaa gtg gcc ctg tcc aac act ggg gag att ccc ttc tat ggc      1056
116 Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly
117                 340                 345                 350
119 aaa gcc atc ccc att gag gcc atc aag ggg gga agg cat ctc atc ttc      1104
120 Lys Ala Ile Pro Ile Glu Ala Ile Lys Gly Gly Arg His Leu Ile Phe
121         355                 360                 365
123 tgc cat tcc aag aag aag tgt gac gag ctc gcc gca aag ctg aca ggc      1152
124 Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Thr Gly
```

```
125     370                    375                    380
127 ctc gga ctc aat gct gta gcg tat tac cgg ggt ctc gat gtg tcc gtc    1200
128 Leu Gly Leu Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val
129 385                    390                    395                400
131 ata ccg act agc gga gac gtc gtt gtc gtg gca aca gac gct cta atg    1248
132 Ile Pro Thr Ser Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met
133                    405                    410                415
135 acg ggc ttt acc ggc gac ttt gac tca gtg atc gac tgc aac aca tgt    1296
136 Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys
137                    420                    425                430
139 gtc acc cag aca gtc gat ttc agc ttg gat ccc acc ttc acc att gag    1344
140 Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu
141             435                    440                    445
143 acg aca acc gtg ccc caa gac gcg gtg tcg cgc tcg cag cgg cga ggt    1392
144 Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly
145     450                    455                    460
147 agg act ggc agg ggc agg agt ggc atc tac agg ttt gtg act cca gga    1440
148 Arg Thr Gly Arg Gly Arg Ser Gly Ile Tyr Arg Phe Val Thr Pro Gly
149 465                    470                    475                480
151 gaa cgg ccc tca ggc atg ttc gac tcc tcg gtc ctg tgt gag tgc tat    1488
152 Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr
153                    485                    490                495
155 gac gca ggc tgc gct tgg tat gag ctc acg ccc gct gag act aca gtc    1536
156 Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Thr Val
157                    500                    505                    510
159 agg ttg cgg gct tac ctg aat aca cca ggg ttg ccc gtc tgc cag gac    1584
160 Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp
161             515                    520                    525
163 cat ctg gag ttc tgg gaa agc gtc ttc aca ggc ctc acc cac ata gat    1632
164 His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp
165     530                    535                    540
167 gcc cac ttc ctg tcc caa acc aag cag gca gga gac aac ttc ccc tac    1680
168 Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr
169 545                    550                    555                560
171 ctg gtg gca tac caa gcc acg gtg tgc gcc agg gct cag gct cca cct    1728
172 Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro
173                    565                    570                    575
175 cca tcg tgg gat caa atg tgg aag tgt ctc ata cgg ctt aaa cct acg    1776
176 Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr
177                    580                    585                    590
179 ctg cac ggg cca aca ccc ctg ctg tat agg cta gga gcc gtt caa aat    1824
180 Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn
181             595                    600                    605
184 gag atc acc ctc aca cat ccc ata acc aaa ttc gtc atg gca tgc atg    1872
185 Glu Ile Thr Leu Thr His Pro Ile Thr Lys Phe Val Met Ala Cys Met
186             610                    615                    620
188 tcg gcc gac ctg gag gtc gtc act agc acc tgg gtg ctg gta ggc gga    1920
189 Ser Ala Asp Leu Glu Val Val Thr Ser Thr Trp Val Leu Val Gly Gly
190 625                    630                    635                640
```

```
192 gtc ctt gca gct ctg gcc gca tat tgc ctg aca acc ggt agt gtg gtc        1968
193 Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Thr Thr Gly Ser Val Val
194             645             650             655
196 att gtg ggt agg atc att ttg tcc ggg agg ccg gct gtt gtt ccc gac        2016
197 Ile Val Gly Arg Ile Ile Leu Ser Gly Arg Pro Ala Val Val Pro Asp
198             660             665             670
200 agg gaa gtc ctc tac cgg gag ttc gat gaa atg gaa gag tgc gcc tca        2064
201 Arg Glu Val Leu Tyr Arg Glu Phe Asp Glu Met Glu Glu Cys Ala Ser
202             675             680             685
204 cac ctc cct tac atc gag caa gga atg cag ctc gcc gag cag ttc aag        2112
205 His Leu Pro Tyr Ile Glu Gln Gly Met Gln Leu Ala Glu Gln Phe Lys
206     690             695             700
208 cag cag gca ctc ggg ttg ctg caa aca gcc acc aag caa gcg gag gcc        2160
209 Gln Gln Ala Leu Gly Leu Leu Gln Thr Ala Thr Lys Gln Ala Glu Ala
210 705             710             715             720
212 gct gct ccc gtg gtg gag tcc agg tgg cgg gcc ctt gag gcc ttc tgg        2208
213 Ala Ala Pro Val Val Glu Ser Arg Trp Arg Ala Leu Glu Ala Phe Trp
214             725             730             735
216 gca aag cac atg tgg aac ttc atc agc ggg ata cag tac tta gca ggc        2256
217 Ala Lys His Met Trp Asn Phe Ile Ser Gly Ile Gln Tyr Leu Ala Gly
218             740             745             750
220 tta tcc act ctg cct ggg aac ccc gcg ata gca tca ctg atg gca ttc        2304
221 Leu Ser Thr Leu Pro Gly Asn Pro Ala Ile Ala Ser Leu Met Ala Phe
222             755             760             765
224 aca gcc tct atc acc agt ccg ctc acc acc cag aat acc ctc cta ttc        2352
225 Thr Ala Ser Ile Thr Ser Pro Leu Thr Thr Gln Asn Thr Leu Leu Phe
226     770             775             780
228 aac atc tta ggg gga tgg gtg gct gct caa ctc gct cct ccc agt gct        2400
229 Asn Ile Leu Gly Gly Trp Val Ala Ala Gln Leu Ala Pro Pro Ser Ala
230 785             790             795             800
232 gct tcg gcc ttc gtg ggt gcc ggc att gcc ggt gcg gcc att ggc agc        2448
233 Ala Ser Ala Phe Val Gly Ala Gly Ile Ala Gly Ala Ala Ile Gly Ser
234             805             810             815
236 ata ggc ctt ggg aag gtg ctt gtg gac att ctg gcg ggc tat gga gcg        2496
237 Ile Gly Leu Gly Lys Val Leu Val Asp Ile Leu Ala Gly Tyr Gly Ala
238             820             825             830
240 ggg gtg gcc ggt gca ctc gtg gct ttt aag gtc atg agc ggc gag gcg        2544
241 Gly Val Ala Gly Ala Leu Val Ala Phe Lys Val Met Ser Gly Glu Ala
242             835             840             845
245 ccc tcc gcc gag gac ctg gtt aac ttg ctc cct gcc atc ctc tcc ccc        2592
246 Pro Ser Ala Glu Asp Leu Val Asn Leu Leu Pro Ala Ile Leu Ser Pro
247     850             855             860
249 ggc gcc ttg gtc gtc ggg atc gtg tgt gca gca atc ctg cgt cgg cac        2640
250 Gly Ala Leu Val Val Gly Ile Val Cys Ala Ala Ile Leu Arg Arg His
251 865             870             875             880
253 gtg ggc ccg gga gag ggg gct gtg cag tgg atg aac cgg ctg ata gcg        2688
254 Val Gly Pro Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu Ile Ala
255             885             890             895
257 ttc gct tcg cgg ggt aac cac gtt tcc ccc acg cac tac gtg cct gag        2736
```

RAW SEQUENCE LISTING   DATE: 12/20/2005
PATENT APPLICATION: US/10/559,431   TIME: 13:16:57

Input Set : A:\pto.da.txt
Output Set: N:\CRF4\12202005\J559431.raw

```
258 Phe Ala Ser Arg Gly Asn His Val Ser Pro Thr His Tyr Val Pro Glu
259         900             905             910
261 agc gac gcc gca gca cgt gta act cag atc ctc tcc agc ctc acc atc         2784
262 Ser Asp Ala Ala Ala Arg Val Thr Gln Ile Leu Ser Ser Leu Thr Ile
263         915             920             925
265 act cag ctg ctg aag agg ctt cac cag tgg att aat gag gac tgc tcc         2832
266 Thr Gln Leu Leu Lys Arg Leu His Gln Trp Ile Asn Glu Asp Cys Ser
267     930             935             940
269 acg cca tgc taa                                                         2844
270 Thr Pro Cys
271 945
274 <210> SEQ ID NO: 2
275 <211> LENGTH: 947
276 <212> TYPE: PRT
277 <213> ORGANISM: Artificial sequence
279 <220> FEATURE:
280 <223> OTHER INFORMATION: sequence coding for NS3NS4
282 <400> SEQUENCE: 2
284 Met Ala Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly
285 1               5               10              15
287 Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Asp Gly
288             20              25              30
290 Glu Val Gln Val Leu Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys
291         35              40              45
293 Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr
294     50              55              60
296 Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp
297 65              70              75              80
299 Gln Asp Leu Val Gly Trp Pro Ala Pro Pro Gly Ala Arg Ser Met Thr
300             85              90              95
302 Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala
303             100             105             110
306 Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu
307         115             120             125
309 Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu
310     130             135             140
312 Leu Cys Pro Ser Gly His Val Val Gly Ile Phe Arg Ala Ala Val Cys
313 145             150             155             160
315 Thr Arg Gly Val Ala Lys Ala Val Asp Phe Ile Pro Val Glu Ser Met
316             165             170             175
318 Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro
319             180             185             190
321 Ala Val Pro Gln Thr Phe Gln Val Ala His Leu His Ala Pro Thr Gly
322         195             200             205
324 Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr
325     210             215             220
327 Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly
329 225             230             235             240
331 Ala Tyr Met Ser Lys Ala His Gly Ile Glu Pro Asn Ile Arg Thr Gly
```

VERIFICATION SUMMARY   DATE: 12/20/2005
PATENT APPLICATION: **US/10/559,431**   TIME: 13:16:58

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\12202005\J559431.raw**

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:30 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:28
L:481 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:479
L:771 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:769
L:997 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:995

Raw Sequence Listing before editing,
for reference only

IFWP

RAW SEQUENCE LISTING	DATE: 12/16/2005	
PATENT APPLICATION: US/10/559,431	TIME: 15:37:52	

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\12162005\J559431.raw**

```
   4 <110> APPLICANT: BIOMERIEUX
   5         INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
   7 <120> TITLE OF INVENTION: Composition comprising the polyprotein NS3/NS4 and the
polypeptide NS5b
   8         of HCV, expression vectors including the corresponding nucleic sequences and
   9         their therapeutic use
  11 <130> FILE REFERENCE: ADENOVIR
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/559,431
C--> 13 <141> CURRENT FILING DATE: 2005-12-05
  13 <160> NUMBER OF SEQ ID NOS: 27
  15 <170> SOFTWARE: PatentIn version 3.1
```

Does Not Comply
Corrected Diskette Needed
(pg-1)

ERRORED SEQUENCES

```
  1565 <210> SEQ ID NO: 27
  1566 <211> LENGTH: 9
  1567 <212> TYPE: PRT
  1568 <213> ORGANISM: Artificial sequence
  1570 <220> FEATURE:
  1571 <223> OTHER INFORMATION: epitope DLM
  1573 <400> SEQUENCE: 27
  1575 Asp Leu Met Gly Tyr Ile Pro Leu Val
  1576 1               5
E--> 1579 ??
E--> 1581 ??
E--> 1583 ??
E--> 1585 ??
E--> 1590 1
```

) deleted

VERIFICATION SUMMARY   DATE: 12/16/2005
PATENT APPLICATION: **US/10/559,431**   TIME: 15:37:54

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\12162005\J559431.raw**

```
L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:30 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:28
L:481 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:479
L:771 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:769
L:997 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:995
L:1579 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1579 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:1581 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:27
L:1581 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1581 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:1583 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:27
L:1583 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1583 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:1585 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:27
L:1585 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1585 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:1590 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:27
```